

Blast 2 Sequences

Exhibit 4

NCBI

E. strez

BLAST 2 sequences

BLAST

Example

Help

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site [Reference](#): Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program ☒ Matrix ☒

Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch: ☐ Use Mega BLAST Strand option ☒Open gap and extension gap penaltiesgap x_dropoff expect word size Filter ☒ Sequence 1 Enter accession or GI or download from file or sequence in FASTA format from: to: Sequence 2 Enter accession or GI or download from file or sequence in FASTA format from: to:

accggaagcgctcagacttggtcg

 Comments and suggestions to blast-help@ncbi.nlm.nih.gov<http://www.ncbi.nlm.nih.gov/blast/bl2seq/bl2.html>

4/28/2002

**Blast 2 Sequences results**

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.3 [Apr-24-2002]Match: Mismatch: gap open: gap extension: x_dropoff: expect: wordsize: Filter ☒

Sequence	gi	Homo sapiens endothelial differentiation, sphingolipid G-protein-	Length 2753
1	13027635	coupled receptor, 1 (EDG1), mRNA	

Sequence	lcl seq_2	Length 25
2		

No significant similarity was found